PCT09

RAW SEQUENCE LISTING   DATE: 05/14/2002
PATENT APPLICATION: US/09/937,636   TIME: 16:28:20

Input Set : A:\X-12652 Seqlist.txt
Output Set: N:\CRF3\05142002\I937636.raw   ENTERED

```
    3 <110> APPLICANT: Eric Wen Su
    4        Jian-Jun Wei
    6 <120> TITLE OF INVENTION: hOB-BP2h COMPOSITIONS, METHODS AND USES THEREOF
    8 <130> FILE REFERENCE: X12652
C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/937,636
C--> 11 <141> CURRENT FILING DATE: 2002-03-05
   13 <160> NUMBER OF SEQ ID NOS: 5
   15 <170> SOFTWARE: PatentIn Ver. 2.1
   17 <210> SEQ ID NO: 1
   18 <211> LENGTH: 1536
   19 <212> TYPE: DNA
   20 <213> ORGANISM: Homo sapiens
   22 <400> SEQUENCE: 1
   23 atgctactgc cactgctgct gtcctcgctg ctgggcgggt cccaggctat ggatgggaga 60
   24 ttctggatac gagtgcagga gtcagtgatg gtgccggagg gcctgtgcat ctctgtgccc 120
   25 tgctctttct cctacccccg acaggactgg acagggtcta ccccagctta tggctactgg 180
   26 ttcaaagcag tgactgagac aaccaagggt gctcctgtgg ccacaaacca ccagagtcga 240
   27 gaggtggaaa tgagcacccg gggccgattc cagctcactg gggatcccgc caaggggaac 300
   28 tgctccttgg tgatcagaga cgcgcagatg caggatgagt cacagtactt ctttcgggtg 360
   29 gagagaggaa gctatgtgag atataatttc atgaacgatg ggttctttct aaaagtaaca 420
   30 gccctgactc agaagcctga tgtctacatc cccgagaccc tggagcccgg gcagccggtg 480
   31 acggtcatct gtgtgtttaa ctgggccttt gaggaatgtc cacccccttc tttctcctgg 540
   32 acggggggctg ccctctcctc ccaaggaacc aaaccaacga cctcccactt ctcagtgctc 600
   33 agcttcacgc ccagacccca ggaccacgac accgacctca cctgccatgt ggacttctcc 660
   34 agaaagggtg tgagcgcaca gaggaccgtc cgactccgtg tggcctatgc ccccagagac 720
   35 cttgttatca gcatttcacg tgacaacacg ccagatcctc cagagaacct gagagtgatg 780
   36 gtttcccaag caaacaggac agtcctggaa aaccttggga cggcacgtc tctcccagta 840
   37 ctggagggcc aaagcctgtg cctggtctgt gtcacacaca gcagccccc agccaggctg 900
   38 agctggaccc agaggggaca ggttctgagc ccctcccagc cctcagaccc cggggtcctg 960
   39 gagctgcctc gggttcaagt ggagcacgaa ggagagttca cctgccacgc tcggcaccca 1020
   40 ctgggctccc agcacgtctc tctcagcctc tccgtgcact ataagaaggg actcatctca 1080
   41 acggcattct ccaatggagc gtttctggga atcggcatca cggctcttct tttcctctgc 1140
   42 ctggccctga tcatcatgaa gattctaccg aagagacgga ctcagacaga aaccccgagg 1200
   43 cccaggttct cccggcacag cacgatcctg gattacatca atgtggtccc gacggctggc 1260
   44 cccctggctc agaagcggaa tcagaaagcc acaccaaaca gtcctcggac ccctcttcca 1320
   45 ccaggtgctc cctccccaga atcaaagaag aaccagaaaa agcagtatca gttgcccagt 1380
   46 ttcccagaac ccaaatcatc cactcaagcc ccagaatccc aggagagcca agaggagctc 1440
   47 cattatgcca cgctcaactt cccaggcgtc agacccaggc ctgaggcccg gatgcccaag 1500
   48 ggcacccagg cggattatgc agaagtcaag ttccaa 1536
   51 <210> SEQ ID NO: 2
   52 <211> LENGTH: 1917
   53 <212> TYPE: DNA
   54 <213> ORGANISM: Homo sapiens
```

RAW SEQUENCE LISTING   DATE: 05/14/2002
PATENT APPLICATION: US/09/937,636   TIME: 16:28:20

Input Set : A:\X-12652 Seqlist.txt
Output Set: N:\CRF3\05142002\I937636.raw

```
56 <400> SEQUENCE: 2
57 atgctactgc cactgctgct gtcctcgctg ctgggcgggt cccaggctat ggatgggaga 60
58 ttctggatac gagtgcagga gtcagtgatg gtgccggagg gcctgtgcat ctctgtgccc 120
59 tgctctttct cctaccccg acaagactgg acagggtcta ccccagctta tggctactgg 180
60 ttcaaagcag tgactgagac aaccaagggt gctcctgtgg ccacaaacca ccagagtcga 240
61 gaggtggaaa tgagcacccg gggccgattc cagctcactg gggatcccgc caaggggaac 300
62 tgctccttgg tgatcagaga cgcgcagatg caggatgagt cacagtactt ctttcgggtg 360
63 gagagaggaa gctatgtgag atataatttc atgaacgatg ggttctttct aaaagtaaca 420
64 gtgctcagct tcacgcccag accccaggac cacaacaccg acctcacctg ccatgtggac 480
65 ttctccagaa agggtgtgag cgcacagagg accgtccgac tccgtgtggc ctatgccccc 540
66 agagaccttg ttatcagcat ttcacgtgac aacacgccag ccctggagcc ccagccccag 600
67 ggaaatgtcc catacctgga agcccaaaaa ggccagttcc tgcggctcct ctgtgctgct 660
68 gacagccagc cccctgccac actgagctgg gtcctgcaga acagagtcct ctcctcgtcc 720
69 catccctggg gccctagacc cctggggctg gagctgcccg gggtgaaggc tggggattca 780
70 gggcgctaca cctgccgagc ggagaacagg cttggctccc agcagcgagc cctggacctc 840
71 tctgtgcagt atcctccaga gaacctgaga gtgatggttt cccaagcaaa caggacagtc 900
72 ctggaaaacc ttgggaacgg cacgtctctc ccagtactgg agggccaaag cctgtgcctg 960
73 gtctgtgtca cacacagcag cccccagcc aggctgagct ggacccagag gggacaggtt 1020
74 ctgagccct cccagccctc agaccccggg gtcctggagc tgcctcgggt tcaagtggag 1080
75 cacgaaggag agttcacctg ccacgctcgg cacccactgg gctcccagca cgtctctctc 1140
76 agcctctccg tgcactactc cccgaagctg ctgggcccct cctgctcctg ggaggctgag 1200
77 ggtctgcact gcagctgctc ctcccaggcc agcccggccc cctctctgcg ctggtggctt 1260
78 ggggaggagc tgctggaggg gaacagcagc caggactcct tcgaggtcac ccccagctca 1320
79 gccgggccct gggccaacag ctccctgagc ctccatggag ggctcagctc cggcctcagg 1380
80 ctccgctgtg aggcctggaa cgtccatggg gcccagagtg gatccatcct gcagctgcca 1440
81 gataagaagg gactcatctc aacggcattc tccaacggag cgtttctggg aatcggcatc 1500
82 acggctcttc ttttcctctg cctggccctg atcatcatga agattctacc gaagagacgg 1560
83 actcagacag aaaccccgag gcccaggttc tcccggcaca gcacgatcct ggattacatc 1620
84 aatgtggtcc cgacggctgg ccccctggct cagaagcgga atcagaaagc cacaccaaac 1680
85 agtcctcgga cccctcttcc accaggtgct ccctccccag aatcaaagaa gaaccagaaa 1740
86 aagcagtatc agttgcccag tttcccagaa cccaaatcat ccactcaagc cccagaatcc 1800
87 caggagagcc aagaggagct ccattatgcc acgctcaact tcccaggcgt cagacccagg 1860
88 cctgaggccc ggatgcccaa gggcacccag gcggattatg cagaagtcaa gttccaa    1917
91 <210> SEQ ID NO: 3
92 <211> LENGTH: 512
93 <212> TYPE: PRT
94 <213> ORGANISM: Homo sapiens
96 <400> SEQUENCE: 3
97 Met Leu Leu Pro Leu Leu Leu Ser Ser Leu Leu Gly Gly Ser Gln Ala
98  1               5                   10                  15
100 Met Asp Gly Arg Phe Trp Ile Arg Val Gln Glu Ser Val Met Val Pro
101             20                  25                  30
103 Glu Gly Leu Cys Ile Ser Val Pro Cys Ser Phe Ser Tyr Pro Arg Gln
104             35                  40                  45
106 Asp Trp Thr Gly Ser Thr Pro Ala Tyr Gly Tyr Trp Phe Lys Ala Val
107     50                  55                  60
109 Thr Glu Thr Thr Lys Gly Ala Pro Val Ala Thr Asn His Gln Ser Arg
110 65                  70                  75                  80
112 Glu Val Glu Met Ser Thr Arg Gly Arg Phe Gln Leu Thr Gly Asp Pro
```

```
113                      85                  90                  95
115 Ala Lys Gly Asn Cys Ser Leu Val Ile Arg Asp Ala Gln Met Gln Asp
116             100                 105                 110
118 Glu Ser Gln Tyr Phe Phe Arg Val Glu Arg Gly Ser Tyr Val Arg Tyr
119         115                 120                 125
121 Asn Phe Met Asn Asp Gly Phe Phe Leu Lys Val Thr Ala Leu Thr Gln
122         130                 135                 140
124 Lys Pro Asp Val Tyr Ile Pro Glu Thr Leu Glu Pro Gly Gln Pro Val
125 145                 150                 155                 160
127 Thr Val Ile Cys Val Phe Asn Trp Ala Phe Glu Glu Cys Pro Pro Pro
128             165                 170                 175
130 Ser Phe Ser Trp Thr Gly Ala Ala Leu Ser Ser Gln Gly Thr Lys Pro
131             180                 185                 190
133 Thr Thr Ser His Phe Ser Val Leu Ser Phe Thr Pro Arg Pro Gln Asp
134         195                 200                 205
136 His Asp Thr Asp Leu Thr Cys His Val Asp Phe Ser Arg Lys Gly Val
137     210                 215                 220
139 Ser Ala Gln Arg Thr Val Arg Leu Arg Val Ala Tyr Ala Pro Arg Asp
140 225                 230                 235                 240
142 Leu Val Ile Ser Ile Ser Arg Asp Asn Thr Pro Asp Pro Pro Glu Asn
143             245                 250                 255
145 Leu Arg Val Met Val Ser Gln Ala Asn Arg Thr Val Leu Glu Asn Leu
146             260                 265                 270
148 Gly Asn Gly Thr Ser Leu Pro Val Leu Glu Gly Gln Ser Leu Cys Leu
149         275                 280                 285
151 Val Cys Val Thr His Ser Ser Pro Pro Ala Arg Leu Ser Trp Thr Gln
152     290                 295                 300
154 Arg Gly Gln Val Leu Ser Pro Ser Gln Pro Ser Asp Pro Gly Val Leu
155 305                 310                 315                 320
157 Glu Leu Pro Arg Val Gln Val Glu His Glu Gly Glu Phe Thr Cys His
158             325                 330                 335
160 Ala Arg His Pro Leu Gly Ser Gln His Val Ser Leu Ser Leu Ser Val
161         340                 345                 350
163 His Tyr Lys Lys Gly Leu Ile Ser Thr Ala Phe Ser Asn Gly Ala Phe
164         355                 360                 365
166 Leu Gly Ile Gly Ile Thr Ala Leu Leu Phe Leu Cys Leu Ala Leu Ile
167     370                 375                 380
169 Ile Met Lys Ile Leu Pro Lys Arg Arg Thr Gln Thr Glu Thr Pro Arg
170 385                 390                 395                 400
172 Pro Arg Phe Ser Arg His Ser Thr Ile Leu Asp Tyr Ile Asn Val Val
173             405                 410                 415
175 Pro Thr Ala Gly Pro Leu Ala Gln Lys Arg Asn Gln Lys Ala Thr Pro
176         420                 425                 430
178 Asn Ser Pro Arg Thr Pro Leu Pro Pro Gly Ala Pro Ser Pro Glu Ser
179         435                 440                 445
181 Lys Lys Asn Gln Lys Lys Gln Tyr Gln Leu Pro Ser Phe Pro Glu Pro
182     450                 455                 460
184 Lys Ser Ser Thr Gln Ala Pro Glu Ser Gln Glu Ser Gln Glu Glu Leu
185 465                 470                 475                 480
```

```
187 His Tyr Ala Thr Leu Asn Phe Pro Gly Val Arg Pro Arg Pro Glu Ala
188             485             490             495
190 Arg Met Pro Lys Gly Thr Gln Ala Asp Tyr Ala Glu Val Lys Phe Gln
191             500             505             510
197 <210> SEQ ID NO: 4
198 <211> LENGTH: 639
199 <212> TYPE: PRT
200 <213> ORGANISM: Homo sapiens
202 <400> SEQUENCE: 4
203 Met Leu Leu Pro Leu Leu Leu Ser Ser Leu Leu Gly Gly Ser Gln Ala
204   1               5               10              15
206 Met Asp Gly Arg Phe Trp Ile Arg Val Gln Glu Ser Val Met Val Pro
207             20              25              30
209 Glu Gly Leu Cys Ile Ser Val Pro Cys Ser Phe Ser Tyr Pro Arg Gln
210             35              40              45
212 Asp Trp Thr Gly Ser Thr Pro Ala Tyr Gly Tyr Trp Phe Lys Ala Val
213       50              55              60
215 Thr Glu Thr Thr Lys Gly Ala Pro Val Ala Thr Asn His Gln Ser Arg
216   65              70              75              80
218 Glu Val Glu Met Ser Thr Arg Gly Arg Phe Gln Leu Thr Gly Asp Pro
219             85              90              95
221 Ala Lys Gly Asn Cys Ser Leu Val Ile Arg Asp Ala Gln Met Gln Asp
222             100             105             110
224 Glu Ser Gln Tyr Phe Phe Arg Val Glu Arg Gly Ser Tyr Val Arg Tyr
225             115             120             125
227 Asn Phe Met Asn Asp Gly Phe Phe Leu Lys Val Thr Val Leu Ser Phe
228             130             135             140
230 Thr Pro Arg Pro Gln Asp His Asn Thr Asp Leu Thr Cys His Val Asp
231 145             150             155             160
233 Phe Ser Arg Lys Gly Val Ser Ala Gln Arg Thr Val Arg Leu Arg Val
234             165             170             175
236 Ala Tyr Ala Pro Arg Asp Leu Val Ile Ser Ile Ser Arg Asp Asn Thr
237             180             185             190
239 Pro Ala Leu Glu Pro Gln Pro Gln Gly Asn Val Pro Tyr Leu Glu Ala
240             195             200             205
242 Gln Lys Gly Gln Phe Leu Arg Leu Leu Cys Ala Ala Asp Ser Gln Pro
243       210             215             220
245 Pro Ala Thr Leu Ser Trp Val Leu Gln Asn Arg Val Leu Ser Ser Ser
246 225             230             235             240
248 His Pro Trp Gly Pro Arg Pro Leu Gly Leu Glu Leu Pro Gly Val Lys
249             245             250             255
251 Ala Gly Asp Ser Gly Arg Tyr Thr Cys Arg Ala Glu Asn Arg Leu Gly
252             260             265             270
254 Ser Gln Gln Arg Ala Leu Asp Leu Ser Val Gln Tyr Pro Pro Glu Asn
255       275             280             285
257 Leu Arg Val Met Val Ser Gln Ala Asn Arg Thr Val Leu Glu Asn Leu
258       290             295             300
260 Gly Asn Gly Thr Ser Leu Pro Val Leu Glu Gly Gln Ser Leu Cys Leu
261 305             310             315             320
```

```
263 Val Cys Val Thr His Ser Ser Pro Pro Ala Arg Leu Ser Trp Thr Gln
264                 325             330             335
266 Arg Gly Gln Val Leu Ser Pro Ser Gln Pro Ser Asp Pro Gly Val Leu
267                 340             345             350
269 Glu Leu Pro Arg Val Gln Val Glu His Glu Gly Glu Phe Thr Cys His
270         355             360             365
272 Ala Arg His Pro Leu Gly Ser Gln His Val Ser Leu Ser Leu Ser Val
273     370             375             380
275 His Tyr Ser Pro Lys Leu Leu Gly Pro Ser Cys Ser Trp Glu Ala Glu
276 385             390             395             400
278 Gly Leu His Cys Ser Cys Ser Ser Gln Ala Ser Pro Ala Pro Ser Leu
279             405             410             415
281 Arg Trp Trp Leu Gly Glu Glu Leu Leu Glu Gly Asn Ser Ser Gln Asp
282         420             425             430
284 Ser Phe Glu Val Thr Pro Ser Ser Ala Gly Pro Trp Ala Asn Ser Ser
285         435             440             445
287 Leu Ser Leu His Gly Gly Leu Ser Ser Gly Leu Arg Leu Arg Cys Glu
288     450             455             460
290 Ala Trp Asn Val His Gly Ala Gln Ser Gly Ser Ile Leu Gln Leu Pro
291 465             470             475             480
293 Asp Lys Lys Gly Leu Ile Ser Thr Ala Phe Ser Asn Gly Ala Phe Leu
294             485             490             495
296 Gly Ile Gly Ile Thr Ala Leu Leu Phe Leu Cys Leu Ala Leu Ile Ile
297         500             505             510
299 Met Lys Ile Leu Pro Lys Arg Arg Thr Gln Thr Glu Thr Pro Arg Pro
300     515             520             525
302 Arg Phe Ser Arg His Ser Thr Ile Leu Asp Tyr Ile Asn Val Val Pro
303     530             535             540
305 Thr Ala Gly Pro Leu Ala Gln Lys Arg Asn Gln Lys Ala Thr Pro Asn
306 545             550             555             560
308 Ser Pro Arg Thr Pro Leu Pro Pro Gly Ala Pro Ser Pro Glu Ser Lys
309             565             570             575
311 Lys Asn Gln Lys Lys Gln Tyr Gln Leu Pro Ser Phe Pro Glu Pro Lys
312             580             585             590
314 Ser Ser Thr Gln Ala Pro Glu Ser Gln Glu Ser Gln Glu Glu Leu His
315         595             600             605
317 Tyr Ala Thr Leu Asn Phe Pro Gly Val Arg Pro Arg Pro Glu Ala Arg
318     610             615             620
320 Met Pro Lys Gly Thr Gln Ala Asp Tyr Ala Glu Val Lys Phe Gln
321 625             630             635
324 <210> SEQ ID NO: 5
325 <211> LENGTH: 58
326 <212> TYPE: PRT
327 <213> ORGANISM: Homo sapiens
329 <400> SEQUENCE: 5
330 Ala Leu Thr Gln Lys Pro Asp Val Tyr Ile Pro Glu Thr Leu Glu Pro
331 1               5               10              15
333 Gly Gln Pro Val Thr Val Ile Cys Val Phe Asn Trp Ala Phe Glu Glu
334             20              25              30
```

VERIFICATION SUMMARY   DATE: 05/14/2002
PATENT APPLICATION: US/09/937,636   TIME: 16:28:21

Input Set : **A:\X-12652 Seqlist.txt**
Output Set: **N:\CRF3\05142002\I937636.raw**

L:10 M:270 C: Current Application Number differs, Replaced Application Number
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date